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MITOGENOME ANNOUNCEMENT



Complete mitochondrial genome of *Goniurosaurus bawanglingensis* (Squamata: Sauria: Eublepharidae)

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ABSTRACT

To date, only a single complete mitochondrial genome sequence has been reported for species in the genus *Goniurosaurus*. In this study, using Illumina sequencing data, we assembled the complete mitochondrial genome of *Goniurosaurus bawanglingensis*, which consists of 16,982 base pairs, comprising 13 protein-coding genes, 2 ribosomal RNA genes, 22 tRNA genes, and non-coding regions (D-Loop), and has an overall A + T content of 61.65%. Using partial sequence data of the 16S rRNA gene of 14 *Goniurosaurus* species, including *G. bawanglingensis*, we reconstructed the phylogeny of the genus *Goniurosaurus*.

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The genus *Goniurosaurus* (Squamata: Sauria: Eublepharidae) comprises 18 species of primarily nocturnal lizards that are mostly associated with rocky/karst topography and are distributed throughout northern Vietnam, southern China, islands in the Beibu Gulf of the South China Sea, and the

Ryukyu Archipelago of Japan (Zhou et al. 2018). To date, however, the taxonomy and phylogeny of the genus *Goniurosaurus* remained unresolved and contentious. Blair et al. (2009) have proposed that further molecular analyses are needed if we wish to gain a better understanding of the

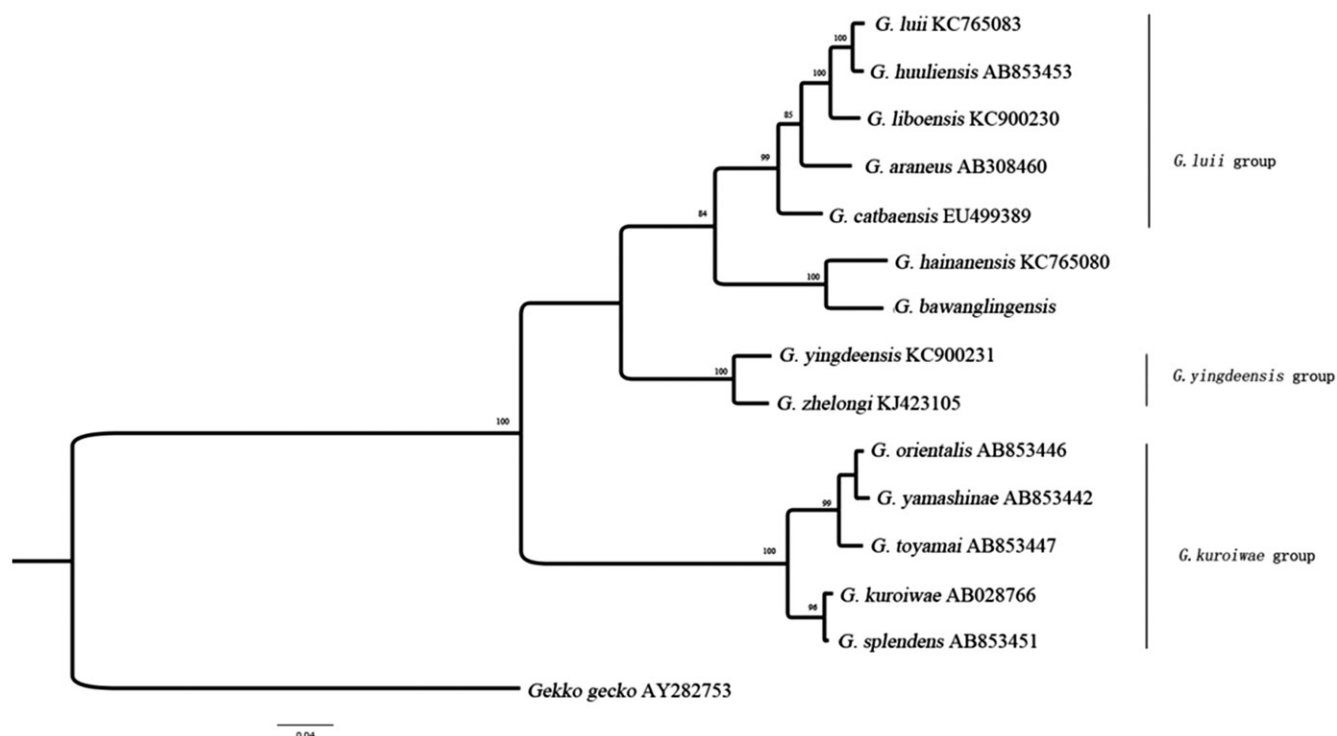


Figure 1. A Bayesian tree based on partial nucleotide sequence data of the 16S rRNA gene of 14 *Goniurosaurus* species.

taxonomy and evolutionary history of this genus, and in this regard, mitogenome analysis has been successfully applied to resolve the phylogenetic relationships among various groups of different taxonomic ranks.

Goniurosaurus bawanglingensis is a species endemic to Hainan Island, China (Grismer et al. 2002), where it mainly inhabits areas surrounding limestone forest caves, near karst cliffs, and primary shrub vegetation on limestone (Grismer et al. 1999, 2002). On the basis of a search of the National Center for Biotechnology Information (NCBI) database, we assumed that the mitogenome of *G. bawanglingensis* has yet to be sequenced, and therefore to further our understanding of species in the genus *Goniurosaurus*, we determined the complete mitogenome sequence of *G. bawanglingensis*.

DNA was extracted using the standard phenol–chloroform method from the tail of a *G. bawanglingensis* specimen (voucher number: HNNU2017052704) collected from the type locality, Bawangling National Nature Reserve, on Hainan Island (19°07′08.10″N, 109°09′07.20″E). The tail and remainder of the specimen have been preserved in 95% ethanol at the College of Life Sciences, Hainan Normal University. The complete mitogenome sequence of *G. bawanglingensis* was determined using high-throughput sequencing technology.

The complete mitogenome of the *G. bawanglingensis* is 16,982 bp in length with a 61.65% A+T content. The genome contains the typical component of 13 protein-coding genes, 2 ribosomal RNA genes, 22 tRNA genes, and non-coding regions (D-Loop). The arrangement of the protein-coding and ribosomal RNA genes is similar to that found in typical vertebrates.

The phylogeny of 14 *Goniurosaurus* species, including *G. bawanglingensis*, was reconstructed based on partial nucleotide sequence data of the 16S rRNA gene using Bayesian inference (BI) methods implemented with MrBayes (version 3.2.2). The resultant BI tree distinctly showed that *G. bawanglingensis* and *G. hainanensis* form a sister group, and that the clade clusters in a monophyletic group with five species of *G. luii* group; *G. yingdeensis*, and *G. zhelongi* constitute the *G. yingdeensis* group; and five *Goniurosaurus* species from the Ryukyu Islands constitute the *G. kuroiwa* group (Figure 1).

Disclosure statement

No potential conflict of interest was reported by the authors.

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